

## Patent Application US/07/923,692A

## SEQUENCE LISTING

See p. 12

## (1) GENERAL INFORMATION:

(i) APPLICANT: Donson, Jon  
Dawson, William O.  
Grantham, George L.  
Turpen, Thomas H.  
Turpen, Ann Myers  
Garger, Stephen J.  
Grill, Laurence K.

(ii) TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS

(iii) NUMBER OF SEQUENCES: 11

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Limbach & Limbach  
(B) STREET: 2001 Ferry Building  
(C) CITY: San Francisco  
(D) STATE: CAL  
(F) ZIP: 94111

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: Patent in Release #1.0, Version #1.25

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 923,692  
(B) FILING DATE: 31-JUL-1992  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 600,244  
(B) FILING DATE: 22-OCT-1990

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 641,617  
(B) FILING DATE: 16-JAN-1991

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 310,881  
(B) FILING DATE: 17-FEB-1989

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 160,766  
(B) FILING DATE: 26-FEB-1988

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 160,771  
(B) FILING DATE: 26-FEB-1988

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53  
54 (vii) PRIOR APPLICATION DATA:  
55 (A) APPLICATION NUMBER: US 347,637  
56 (B) FILING DATE: 05-MAY-1989  
57  
58 (vii) PRIOR APPLICATION DATA:  
59 (A) APPLICATION NUMBER: US 363,138  
60 (B) FILING DATE: 08-JUN-1989  
61  
62 (vii) PRIOR APPLICATION DATA:  
63 (A) APPLICATION NUMBER: US 219,279  
64 (B) FILING DATE: 15-JUL-1988  
65  
66 (viii) ATTORNEY/AGENT INFORMATION:  
67 (A) NAME: Halluin, Albert P.  
68 (B) REGISTRATION NUMBER: 28,957  
69 (C) REFERENCE/DOCKET NUMBER: BIOG-20121 USA  
70  
71 (ix) TELECOMMUNICATION INFORMATION:  
72 (A) TELEPHONE: 415-433-4150  
73 (B) TELEFAX: 415-433-8716  
74  
75  
76 (2) INFORMATION FOR SEQ ID NO: 1:  
77  
78 (i) SEQUENCE CHARACTERISTICS:  
79 (A) LENGTH: 4 amino acids  
80 (B) TYPE: amino acid  
81 (D) TOPOLOGY: linear  
82  
83 (ii) MOLECULE TYPE: peptide  
84  
85 (iii) HYPOTHETICAL: NO  
86  
87 (iv) ANTI-SENSE: NO  
88  
89 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
90  
91 Pro Xaa Gly Pro  
92 1  
93  
94 (2) INFORMATION FOR SEQ ID NO: 2:  
95  
96 (i) SEQUENCE CHARACTERISTICS:  
97 (A) LENGTH: 13 base pairs  
98 (B) TYPE: nucleic acid  
99 (C) STRANDEDNESS: single  
100 (D) TOPOLOGY: linear  
101  
102 (ii) MOLECULE TYPE: DNA (genomic)  
103  
104 (iii) HYPOTHETICAL: NO

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105  
106 (iv) ANTI-SENSE: NO  
107  
108 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
109  
110 GGGTACCTGG GCC 13  
111  
112  
113  
114 (2) INFORMATION FOR SEQ ID NO: 3:  
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116 (i) SEQUENCE CHARACTERISTICS:  
117 (A) LENGTH: 886 base pairs  
118 (B) TYPE: nucleic acid  
119 (C) STRANDEDNESS: single  
120 (D) TOPOLOGY: linear  
121  
122 (ii) MOLECULE TYPE: DNA (genomic)  
123  
124 (iii) HYPOTHETICAL: NO  
125  
126 (iv) ANTI-SENSE: NO  
127  
128 (vi) ORIGINAL SOURCE:  
129 (A) ORGANISM: Chinese cucumber  
130  
131 (vii) IMMEDIATE SOURCE:  
132 (B) CLONE: alpha-trichosanthin  
133  
134 (ix) FEATURE:  
135 (A) NAME/KEY: CDS (B) LOCATION: 8. .877  
136 (B) LOCATION: 8. .877  
137  
138 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
139  
140 CTCGAGG ATG ATC AGA TTC TTA GTC CTC TCT TTG CTA ATT CTC ACC CTC 49  
141  
142 Met Ile Arg Phe Leu Val Leu Ser Leu Leu Ile Leu Thr Leu  
143 1 5 10  
144  
145 TTC CTA ACA ACT CCT GCT GTG GAG GGC GAT GTT AGC TTC CGT TTA TCA 97  
146  
147 Phe Leu Thr Thr Pro Ala Val Glu Gly Asp Val Ser Phe Arg Leu Ser  
148 15 20 25 30  
149  
150 GGT GCA ACA AGC AGT TCC TAT GGA GTT TTC ATT TCA AAT CTG AGA AAA 145  
151  
152 Gly Ala Thr Ser Ser Ser Tyr Gly Val Phe Ile Ser Asn Leu Arg Lys  
153 35 40 45  
154  
155 GCT CTT CCA AAT GAA AGG AAA CTG TAC GAT ATC CCT CTG TTA CGT TCC 193  
156

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157 Ala Leu Pro Asn Glu Arg Lys Leu Tyr Asp Ile Pro Leu Leu Arg Ser
158      50      55      60
159
160 TCT CTT CCA GGT TCT CAA CGC TAC GCA TTG ATC CAT CTC ACA AAT TAC      241
161
162 Ser Leu Pro Gly Ser Gln Arg Tyr Ala Leu Ile His Leu Thr Asn Tyr
163      65      70      75
164
165 GCC GAT GAA ACC ATT TCA GTG GCC ATA GAC GTA ACG AAC GTC TAT ATT      289
166
167 Ala Asp Glu Thr Ile Ser Val Ala Ile Asp Val Thr Asn Val Tyr Ile
168      80      85      90
169
170 ATG GGA TAT CGC GCT GGC GAT ACA TCC TAT TTT TTC AAC GAG GCT TCT      337
171
172 Met Gly Tyr Arg Ala Gly Asp Thr Ser Tyr Phe Phe Asn Glu Ala Ser
173      95      100      105      110
174
175 GCA ACA GAA GCT GCA AAA TAT GTA TTC AAA GAC GCT ATG CGA AAA GTT      385
176
177 Ala Thr Glu Ala Ala Lys Tyr Val Phe Lys Asp Ala Met Arg Lys Val
178      115      120      125
179
180 ACG CTT CCA TAT TCT GGC AAT TAC GAA AGG CTT CAA ACT GCT GCG GGC      433
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182 Thr Leu Pro Tyr Ser Gly Asn Tyr Glu Arg Leu Gln Thr Ala Ala Gly
183      130      135      140
184
185 AAA ATA AGG GAA AAT ATT CCG CTT GGA CTC CCA GCT TTG GAC AGT GCC      481
186
187 Lys Ile Arg Glu Asn Ile Pro Leu Gly Leu Pro Ala Leu Asp Ser Ala
188      145      150      155
189
190 ATT ACC ACT TTG TTT TAC TAC AAC GCC AAT TCT GCT GCG TCG GCA CTT      529
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192 Ile Thr Thr Leu Phe Tyr Tyr Asn Ala Asn Ser Ala Ala Ser Ala Leu
193      160      165      170
194
195 ATG GTA CTC ATT CAG TCG ACG TCT GAG GCT GCG AGG TAT AAA TTT ATT      577
196
197 Met Val Leu Ile Gln Ser Thr Ser Glu Ala Ala Arg Tyr Lys Phe Ile
198      175      180      185      190
199
200 GAG CAA CAA ATT GGG AAG CGC GTT GAC AAA ACC TTC CTA CCA AGT TTA      625
201
202 Glu Gln Gln Ile Gly Lys Arg Val Asp Lys Thr Phe Leu Pro Ser Leu
203      195      200      205
204
205 GCA ATT ATA AGT TTG GAA AAT AGT TGG TCT GCT CTC TCC AAG CAA ATT      673
206
207 Ala Ile Ile Ser Leu Glu Asn Ser Trp Ser Ala Leu Ser Lys Gln Ile
208      210      215      220

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209  
210 CAG ATA GCG AGT ACT AAT AAT GGA CAG TTT GAA ACT CCT GTT GTG CTT 721  
211  
212 Gln Ile Ala Ser Thr Asn Asn Gly Gln Phe Glu Thr Pro Val Val Leu  
213 225 230 235  
214  
215 ATA AAT GCT CAA AAC CAA CGA GTC ATG ATA ACC AAT GTT GAT GCT GGA 769  
216  
217 Ile Asn Ala Gln Asn Gln Arg Val Met Ile Thr Asn Val Asp Ala Gly  
218 240 245 250  
219  
220 GTT GTA ACC TCC AAC ATC GCG TTG CTG CTG AAT CGA AAC AAT ATG GCA 817  
221  
222 Val Val Thr Ser Asn Ile Ala Leu Leu Leu Asn Arg Asn Asn Met Ala  
223 255 260 265 270  
224  
225 GCC ATG GAT GAC GAT GTT CCT ATG ACA CAG AGC TTT GGA TGT GGA AGT 865  
226  
227 Ala Met Asp Asp Asp Val Pro Met Thr Gln Ser Phe Gly Cys Gly Ser  
228 275 280 285  
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230 TAT GCT ATT TAGTAACTCG AG 886  
231  
232 Tyr Ala Ile  
233 290  
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235  
236 (2) INFORMATION FOR SEQ ID NO:4:  
237  
238 (i) SEQUENCE CHARACTERISTICS:  
239 (A) LENGTH: 289 amino acids  
240 (B) TYPE: amino acid  
241 (D) TOPOLOGY: linear  
242  
243 (ii) MOLECULE TYPE: protein  
244  
245 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
246  
247  
248 Met Ile Arg Phe Leu Val Leu Ser Leu Leu Ile Leu Thr Leu Phe Leu  
249 1 5 10 15  
250  
251 Thr Thr Pro Ala Val Glu Gly Asp Val Ser Phe Arg Leu Ser Gly Ala  
252 20 25 30  
253  
254 Thr Ser Ser Ser Tyr Gly Val Phe Ile Ser Asn Leu Arg Lys Ala Leu  
255 35 40 45  
256  
257 Pro Asn Glu Arg Lys Leu Tyr Asp Ile Pro Leu Leu Arg Ser Ser Leu  
258 50 55 60  
259  
260 Pro Gly Ser Gln Arg Tyr Ala Leu Ile His Leu Thr Asn Tyr Ala Asp

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261      65              70              75              80
262
263 Glu Thr Ile Ser Val Ala Ile Asp Val Thr Asn Val Tyr Ile Met Gly
264              85              90              95
265
266 Tyr Arg Ala Gly Asp Thr Ser Tyr Phe Phe Asn Glu Ala Ser Ala Thr
267              100              105              110
268
269 Glu Ala Ala Lys Tyr Val Phe Lys Asp Ala Met Arg Lys Val Thr Leu
270              115              120              125
271
272 Pro Tyr Ser Gly Asn Tyr Glu Arg Leu Gln Thr Ala Ala Gly Lys Ile
273              130              135              140
274
275 Arg Glu Asn Ile Pro Leu Gly Leu Pro Ala Leu Asp Ser Ala Ile Thr
276              145              150              155              160
277
278 Thr Leu Phe Tyr Tyr Asn Ala Asn Ser Ala Ala Ser Ala Leu Met Val
279              165              170              175
280
281 Leu Ile Gln Ser Thr Ser Glu Ala Ala Arg Tyr Lys Phe Ile Glu Gln
282              180              185              190
283
284 Gln Ile Gly Lys Arg Val Asp Lys Thr Phe Leu Pro Ser Leu Ala Ile
285              195              200              205
286
287 Ile Ser Leu Glu Asn Ser Trp Ser Ala Leu Ser Lys Gln Ile Gln Ile
288              210              215              220
289
290 Ala Ser Thr Asn Asn Gly Gln Phe Glu Thr Pro Val Val Leu Ile Asn
291              225              230              235              240
292
293 Ala Gln Asn Gln Arg Val Met Ile Thr Asn Val Asp Ala Gly Val Val
294              245              250              255
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296 Thr Ser Asn Ile Ala Leu Leu Leu Asn Arg Asn Asn Met Ala Ala Met
297              260              265              270
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299 Asp Asp Asp Val Pro Met Thr Gln Ser Phe Gly Cys Gly Ser Tyr Ala
300              275              280              285
301
302 Ile
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304
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## (2) INFORMATION FOR SEQ ID NO: 5:

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307 (i) SEQUENCE CHARACTERISTICS:
308 (A) LENGTH: 1450 base pairs
309 (B) TYPE: nucleic acid
310 (C) STRANDEDNESS: single
311 (D) TOPOLOGY: linear
312
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313 (ii) MOLECULE TYPE: DNA (genomic)  
314  
315 (iii) HYPOTHETICAL: NO  
316  
317 (iv) ANTI-SENSE: NO  
318  
319 (vi) ORIGINAL SOURCE:  
320 (A) ORGANISM: *Oryza sativa*  
321  
322 (vii) IMMEDIATE SOURCE:  
323 (B) CLONE: alpha-amylase  
324  
325 (ix) FEATURE:  
326 (A) NAME/KEY: CDS (B) LOCATION: 12. .1316  
327 (B) LOCATION: 12. .1316  
328  
329 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
330  
331 CCTCGAGGTG C ATG CAG GTG CTG AAC ACC ATG GTG AAC A CAC TTC TTG 48  
332  
333 Met Gln Val Leu Asn Thr Met Val Asn Lys His Phe Leu  
334 1 5 10  
335  
336 TCC CTT TCG GTC CTC ATC GTC CTC CTT GGC CTC TCC TCC AAC TTG ACA 96  
337  
338 Ser Leu Ser Val Leu Ile Val Leu Leu Gly Leu Ser Ser Asn Leu Thr  
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340  
341 GCC GGG CAA GTC CTG TTT CAG GGA TTC AAC TGG GAG TCG TGG AAG GAG 144  
342  
343 Ala Gly Gln Val Leu Phe Gln Gly Phe Asn Trp Glu Ser Trp Lys Glu  
344 30 35 40 45  
345  
346 AAT GGC GGG TGG TAC AAC TTC CTG ATG GGC AAG GTG GAC GAC ATC GCC 192  
347  
348 Asn Gly Gly Trp Tyr Asn Phe Leu Met Gly Lys Val Asp Asp Ile Ala  
349 50 55 60  
350  
351 GCA GCC GGC ATC ACC CAC GTC TGG CTC CCT CCG CCG TCT CAC TCT GTC 240  
352  
353 Ala Ala Gly Ile Thr His Val Trp Leu Pro Pro Pro Ser His Ser Val  
354 65 70 75  
355  
356 GGC GAG CAA GGC TAC ATG CCT GGG CGG CTG TAC GAT CTG GAC GCG TCT 288  
357  
358 Gly Glu Gln Gly Tyr Met Pro Gly Arg Leu Tyr Asp Leu Asp Ala Ser  
359 80 85 90  
360  
361 AAG TAC GGC AAC GAG GCG CAG CTC AAG TCG CTG ATC GAG GCG TTC CAT 336  
362  
363 Lys Tyr Gly Asn Glu Ala Gln Leu Lys Ser Leu Ile Glu Ala Phe His  
364 95 100 105

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365  
366 GGC AAG GGC GTC CAG GTG ATC GCC GAC ATC GTC ATC AAC CAC CGC ACG 384  
367  
368 Gly Lys Gly Val Gln Val Ile Ala Asp Ile Val Ile Asn His Arg Thr  
369 110 115 120 125  
370  
371 GCG GAG CAC AAG GAC GGC CGC GGC ATC TAC TGC CTC TTC GAG GGC GGG 432  
372  
373 Ala Glu His Lys Asp Gly Arg Gly Ile Tyr Cys Leu Phe Glu Gly Gly  
374 130 135 140  
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376 ACG CCC GAC TCC CGC CTC GAC TGG GGC CCG CAC ATG ATC TGC CGC GAC 480  
377  
378 Thr Pro Asp Ser Arg Leu Asp Trp Gly Pro His Met Ile Cys Arg Asp  
379 145 150 155  
380  
381 GAC CCC TAC GGC CAT GGC ACC GGC AAC CCG GAC ACC GGC GCC GAC TTC 528  
382  
383 Asp Pro Tyr Gly Asp Gly Thr Gly Asn Pro Asp Thr Gly Ala Asp Phe  
384 160 165 170  
385  
386 GCC GCC GCG CCG GAC ATC GAC CAC CTC AAC AAG CGC GTC CAG CGG GAG 576  
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388 Ala Ala Ala Pro Asp Ile Asp His Leu Asn Lys Arg Val Gln Arg Glu  
389 175 180 185  
390  
391 CTC ATT GGC TGG CTC GAC TGG CTC AAG ATG GAC ATC GGC TTC GAC GCG 624  
392  
393 Leu Ile Gly Trp Leu Asp Trp Leu Lys Met Asp Ile Gly Phe Asp Ala  
394 190 195 200 205  
395  
396 TGG CGC CTC GAC TTC GCC AAG GGC TAC TCC GCC GAC ATG GCA AAC ATC 672  
397  
398 Trp Arg Leu Asp Phe Ala Lys Gly Tyr Ser Ala Asp Met Ala Lys Ile  
399 210 215 220  
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401 TAC ATC GAC GCC ACC GAG CCG AGC TTC GCC GTG CCC GAG ATA TCG ACG 720  
402  
403 Tyr Ile Asp Ala Thr Glu Pro Ser Phe Ala Val Ala Glu Ile Trp Thr  
404 225 230 235  
405  
406 TCC ATG GCG AAC GGC GGG GAC GGC AAG CCG AAC TAC GAC CAG AAC GCG 768  
407  
408 Ser Met Ala Asn Gly Gly Asp Gly Lys Pro Asn Tyr Asp Gln Asn Ala  
409 240 245 250  
410  
411 CAC CGG CAG GAG CTG GTC AAC TGG GTC GAT CGT GTC GGC GGC GCC AAC 816  
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413 His Arg Gln Glu Leu Val Asn Trp Val Asp Arg Val Gly Gly Ala Asn  
414 255 260 265  
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416 ACC AAC GGC ACG GCG TTC GAC TTC ACC ACC AAG GGC ATC CTC AAC GTC 864



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417
418 Ser Asn Gly Thr Ala Phe Asp Phe Thr Thr Lys Gly Ile Leu Asn Val
419 270                275                280                285
420
421 GCC GTG GAG GGC GAG CTG TGG CGC CTC CGC GGC GAG GAC GGC AAG GCG      912
422
423 Ala Val Glu Gly Glu Leu Trp Arg Leu Arg Gly Glu Asp Gly Lys Ala
424                290                295                300
425
426 CCC GGC ATG ATC GGG TGC TGG CCG GCC AAG GCG ACG ACC TTC GTC GAC      960
427
428 Pro Gly Met Ile Gly Trp Trp Pro Ala Lys Ala Thr Thr Phe Val Asp
429                305                310                315
430
431 AAC CAC GAC ACC GGC TCG ACG CAG CAC CTG TGG CCG TTC CCC TCC GAC      1008
432
433 Asn His Asp Thr Gly Ser Thr Gln His Leu Trp Pro Phe Pro Ser Asp
434                320                325                330
435
436 AAG GTC ATG CAG GGC TAC GCA TAC ATC CTC ACC CAC CCC GGC AAC CCA      1056
437
438 Lys Val Met Gln Gly Tyr Ala Tyr Ile Leu Thr His Pro Gly Asn Pro
439                335                340                345
440
441 TGC ATC TTG TAC GAC CAT TTC TTC GAT TGG GGT CTC AAG GAG GAG ATC      1104
442
443 Cys Ile Phe Tyr Asp His Phe Phe Asp Trp Gly Leu Lys Glu Glu Ile
444 350                355                360                365
445
446 GAG CGC CTG GTG TCA ATC AGA AAC CGG CAG GGG ATC CAC CCG GCG AGC      1152
447
448 Glu Arg Leu Val Ser Ile Arg Asn Arg Gln Gly Ile His Pro Ala Ser
449                370                375                380
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451 GAG CTG CGC ATC ATG GAA GCT GAC AGC GAT CTC TAC CTC GCG GAG ATC      1200
452
453 Glu Leu Arg Ile Met Glu Ala Asp Ser Asp Leu Tyr Leu Ala Glu Ile
454                385                390                395
455
456 GAT GGC AAG GTG ATC ACA AAG ATT GGA CCA AGA TAC GAC GTC GAA CAC      1248
457
458 Asp Gly Lys Val Ile Thr Lys Ile Gly Pro Arg Tyr Asp Val Glu His
459                400                405                410
460
461 CTC ATC CCC GAA GGC TTC CAG GTC GTC GCG CAC GGT GAT GGC TAC GCA      1296
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463 Leu Ile Pro Glu Gly Phe Gln Val Val Ala His Gly Asp Gly Tyr Ala
464 415                420                425
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466 ATC TGG GAG AAA ATC TGAGCGCACG ATGACGAGAC TCTCAGTTTA GCAGATTTAA      1351
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468 Ile Trp Glu Lys LIe

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469 430 435  
470  
471 CCTGCGATTT TTACCCTGAC CGGTATACGT ATATACGTGC CGGCAACGAG CTGTATCCGA 1411  
472  
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474 TCCGAATTAC GGATGCAATT GTCCACGAAG TCCTCGAGG 1450  
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478 (2) INFORMATION FOR SEQ ID NO: 6:  
479  
480 (i) SEQUENCE CHARACTERISTICS:  
481 (A) LENGTH: 434 amino acids  
482 (B) TYPE: amino acid  
483 (D) Topology: linear  
484  
485 (ii) MOLECULE TYPE: protein  
486  
487 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
488  
489 Met Gln Val Leu Asn Thr Met Val Asn Lys His Phe Leu Ser Leu Ser  
490 1 5 10 15  
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492 Val Leu Ile Val Leu Leu Gly Leu Ser Ser Asn Leu Thr Ala Gly Gln  
493 20 25 30  
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495 Val Leu Phe Gln Gly Phe Asn Trp Glu Ser Trp Lys Glu Asn Gly Gly  
496 35 40 45  
497  
498 Trp Tyr Asn Phe Leu Met Gly Lys Val Asp Asp Ile Ala Ala Ala Gly  
499 50 55 60  
500  
501 Ile Thr His Val Trp Leu Pro Pro Pro Ser His Ser Val Gly Glu Gln  
502 65 70 75 80  
503  
504 Gly Tyr Met Pro Gly Arg Leu Tyr Asp Leu Asp Ala Ser Lys Tyr Gly  
505 85 90 95  
506  
507 Asn Glu Ala Gln Leu Lys Ser Leu Ile Glu Ala Phe His Gly Lys Gly  
508 100 105 110  
509  
510 Val Gln Val Ile Ala Asp Ile Val Ile Asn His Arg Thr Ala Glu His  
511 115 120 125  
512  
513 Lys Asp Gly Arg Gly Ile Tyr Cys Leu Phe Glu Gly Gly Thr Pro Asp  
514 130 135 140  
515  
516 Ser Arg Leu Asp Trp Gly Pro His Met Ile Cys Arg Asp Asp Pro Tyr  
517 145 150 155 160  
518  
519 Gly Asp Gly Thr Gly Asn Pro Asp Thr Gly Ala Asp Phe Ala Ala Ala  
520 165 170 175

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521  
522 Pro Asp Ile Asp His Leu Asn Lys Arg Val Gln Arg Glu Leu Ile Gly  
523 180 185 190  
524  
525 Trp Leu Asp Trp Leu Lys Met Asp Ile Gly Phe Asp Ala Trp Arg Leu  
526 195 200 205  
527  
528 Asp Phe Ala Lys Gly Tyr Ser Ala Asp Met Ala Lys Ile Tyr Ile Asp  
529 210 215 220  
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531 Ala Thr Glu Pro Ser Phe Ala Val Ala Glu Ile Trp Thr Ser Met Ala  
532 225 230 235 240  
533  
534 Asn Gly Gly Asp Gly Lys Pro Asn Tyr Asp Gln Asn Ala His Arg Gln  
535 245 250 255  
536  
537 Glu Leu Val Asn Trp Val Asp Arg Val Gly Gly Ala Asn Ser Asn Gly  
538 260 265 270  
539  
540 Thr Ala Phe Asp Phe Thr Thr Lys Gly Ile Leu Asn Val Ala Val Glu  
541 275 280 285  
542  
543 Gly Glu Leu Trp Arg Leu Arg Gly Glu Asp Gly Lys Ala Pro Gly Met  
544 290 295 300  
545  
546 Ile Gly Trp Trp Pro Ala Lys Ala Thr Thr Phe Val Asp Asn His Asp  
547 305 310 315 320  
548  
549 Thr Gly Ser Thr Gln His Leu Trp Pro Phe Pro Ser Asp Lys Val Met  
550 325 330 335  
551  
552 Gln Gly Tyr Ala Tyr Ile Leu Thr His Pro Gly Asn Pro Cys Ile Phe  
553 340 345 350  
554  
555 Tyr Asp His Phe Phe Asp Trp Gly Leu Lys Glu Glu Ile Glu Arg Leu  
556 355 360 365  
557  
558 Val Ser Ile Arg Asn Arg Gln Gly Ile His Pro Ala Ser Glu Leu Arg  
559 370 375 380  
560  
561 Ile Met Glu Ala Asp Ser Asp Leu Tyr Leu Ala Glu Ile Asp Gly Lys  
562 385 390 395 400  
563  
564 Val Ile Thr Lys Ile Gly Pro Arg Tyr Asp Val Glu His Leu Ile Pro  
565 405 410 415  
566  
567 Glu Gly Phe Gln Val Val Ala His Gly Asp Gly Tyr Ala Ile Trp Glu  
568 420 425 430  
569  
570 Lys Ile  
571  
572

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573 (2) INFORMATION FOR SEQ ID NO:7:

574

575 (i) SEQUENCE CHARACTERISTICS:

576 (A) LENGTH: 709 base pairs

577 (B) TYPE: nucleic acid

578 (G) STRANDEDNESS: single

579 (D) TOPOLOGY: linear

580

581 (ii) MOLECULE TYPE: cDNA to mRNA

582

583 (iii) HYPOTHETICAL: NO

584

585 (iv) ANTI-SENSE: NO

586

587 (vi) ORIGINAL SOURCE:

588 (A) ORGANISM: Homo sapiens

589

590 (vii) IMMEDIATE SOURCE:

591 (B) CLONE: alpha-hemoglobin

592

593 (ix) FEATURE:

594 (A) NAME/KEY: transit\_peptide (B) LOCATION: 26..241

595 (B) LOCATION: 26..241

596

597 (ix) FEATURE:

598 (A) NAME/KEY: CDS

599 (B) LOCATION: 245..670

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601 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

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603 CTCGAGGGCA TCTGATCTTT CAAGAATGGC ACAAATTAAC AACATGGCAC AAGGGATACA 60

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605 AACCCTTAAT CCCAATTCCA ATTTCCATAA ACCCCAAGTT CCTAAATCTT CAAGTTTTCT 120

606

607 TGTTTTTGGG TGAAAAAAC TGAAAATTC AGCAAATTCT ATGTTGGTTT TGAAAAAAGA 180

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609 TTCAATTTTT ATGCAAAAGT TTTGTTCTTT TAGGATTTCA GCAGGTGGTA GAGTTTCTTG 240

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611 CATG GTG CTG TCT CCT GCC GAC AAG ACC AAC GTC AAG GCC GCC TGG GGC 289

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613 Val Leu Ser Pro Ala Asp Lys Thr Asn Val Lys Ala Ala Trp Cly

614 1 5 10 15

615

616 AAG GTT GGC GCG CAC GCT GGC GAG TAT GGT GCG GAG GCC CTG GAG AGG 337

617

618 Lys Val Gly Ala His Ala Gly Glu Tyr Gly Ala Glu Ala Leu Glu Arg

619 20 25 30

620

621 ATG TTC CTG TCC TTC CCC ACC ACC AAG ACC TAC TTC CCG CAC TTC GAC 385

622

623 Met Phe Leu Ser Phe Pro Thr Thr Lys Thr Tyr Phe Pro His Phe Asp

624 35 40 45

Only 677 are listed  
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625  
626 CTG AGC CAC GGC TCT GCC CAG GTT AAG GGC CAC GGC AAG AAG GTG GCC 433  
627  
628 Leu Ser His Gly Ser Ala Gln Val Lys Gly His Gly Lys Lys Val Ala  
629 50 55 60  
630  
631 GAC GCG CTG ACC AAC GCC GTG GCG CAC GTG GAC GAC ATG CCC AAC GCG 481  
632  
633 Asp Ala Leu Thr Asn Ala Val Ala His Val Asp Asp Met Pro Asn Ala  
634 65 70 75  
635  
636 CTG TCC GCC CTG AGC GAC CTG CAC GCG CAC AAG CTT CGG GTG GAC CCG 529  
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638 Leu Ser Ala Leu Ser Asp Leu His Ala His Lys Leu Arg Val Asp Pro  
639 80 85 90 95  
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641 GTC AAC TTC AAG CTC CTA AGC CAC TGC CTG CTG GTG ACC CTG GCC GCC 577  
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643 Val Asn Phe Lys Leu Leu Ser His Cys Leu Leu Val Thr Leu Ala Ala  
644 100 105 110  
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646 CAC CTC CCC GCC GAG TTC ACC CCT GCG GTG CAC GCC TCC CTG GAC AAG 625  
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648 His Leu Pro Ala Glu Phe Thr Pro Ala Val His Ala Ser Leu Asp Lys  
649 115 120 125  
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651 TTC CTG GCT TCT GTG AGC ACC GTG CTG ACC TCC AAA TAC CGT TAAGCTGGAG 677  
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653 Phe Leu Ala Ser Val Ser Thr Val Leu Thr Ser Lys Tyr Arg  
654 130 135 140  
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657 CCTCGGTAGC CGTTCCTCCT GCCCGGTCGA CC 709  
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660 (2) INFORMATION FOR SEQ ID NO:8:  
661  
662 (i) SEQUENCE CHARACTERISTICS:  
663 (A) LENGTH: 141 amino acids  
664 (B) TYPE: amino acid  
665 (D) TOPOLOGY: linear  
666  
667 (ii) MOLECULE TYPE: protein  
668  
669  
670 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:8:  
671  
672 Val Leu Ser Pro Ala Asp Lys Thr Asn Val Lys Ala Ala Trp Gly Lys  
673 1 5 10 15  
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675 Val Gly Ala His Ala Gly Glu Tyr Gly Ala Glu Ala Leu Glu Arg Met  
676 20 25 30

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677  
678 Phe Leu Ser Phe Pro Thr Thr Lys Thr Tyr Phe Pro His Phe Asp Leu  
679 35 40 45  
680  
681 Ser His Gly Ser Ala Gln Val Lys Gly His Gly Lys Lys Val Ala Asp  
682 50 55 60  
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684 Ala Leu Thr Asn Ala Val Ala His Val Asp Asp Met Pro Asn Ala Leu  
685 65 70 75 80  
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687 Ser Ala Leu Ser Asp Leu His Ala His Lys Leu Arg Val Asp Pro Val  
688 85 90 95  
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690 Asn Phe Lys Leu Leu Ser His Cys Leu Leu Val Thr Leu Ala Ala His  
691 100 105 110  
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693 Leu Pro Ala Glu Phe Thr Pro Ala Val His Ala Ser Leu Asp Lys Phe  
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696 Leu Ala Ser Val Ser Thr Val Leu Thr Ser Lys Tyr Arg  
697 130 135 140  
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## 700 (2) INFORMATION FOR SEQ ID NO:9:

701  
702 (i) SEQUENCE CHARACTERISTICS:  
703 (A) LENGTH: 743 base pairs  
704 (B) TYPE: nucleic acid  
705 (C) STRANDEDNESS: single  
706 (D) TOPOLOGY: linear  
707  
708 (ii) MOLECULE TYPE: cDNA to mRNA  
709  
710 (iii) HYPOTHETICAL: NO  
711  
712 (iv) ANTI-SENSE: NO  
713  
714 (vi) ORIGINAL SOURCE:  
715 (A) ORGANISM: Homo sapiens  
716  
717 (vii) IMMEDIATE SOURCE:  
718 (B) CLONE: beta-hemoglobin  
719  
720 (ix) FEATURE:  
721 (A) NAME/KEY: transit\_peptide (B) LOCATION: 26..241  
722 (B) LOCATION: 26..241  
723  
724 (ix) FEATURE:  
725 (A) NAME/KEY: CDS  
726 (B) LOCATION: 245..685  
727  
728 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

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761      65              70              75
762
763 AAC CTC AAG GGC ACC TTT GCC ACC CTG AGT GAG CTG CAC TGT GAC AAG      529
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765 Asn Leu Lys Gly Thr Phe Ala Thr Leu Ser Glu Leu His Cys Asp Lys
766      80              85              90              95
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768 CTG CAC GTG GAT CCT GAG AGC TTC AGG CTC CTA GGC AAC GTG CTG GTC      577
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770 Leu His Val Asp Pro Glu Ser Phe Arg Leu Leu Gly Asn Val Leu Val
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773 TGT GTG CTG GCG CAT CAC TTT GGC AAA GAA TTC ACC CCA CCA GTG CAG      625
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775 Cys Val Leu Ala His His Phe Gly Lys Glu Phe Thr Pro Pro Val Gln
776      115              120              125
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778 GCT GCC TAT CAG AAA GTG GTG GCT GGT GTG GCT AAT GCC CTG GCC CAC      673
779
780 Ala Ala Tyr Gln Lys Val Val Ala Gly Val Ala Asn Ala Leu Ala His

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783 AAG TAT CAC TAAGCTCGCT TTCTTGCTGT CCAATTTCTA TTAAAGGTTT                   722  
784  
785 Lys Tyr His  
786       145  
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788 CTTTGTGGGG TCGAGGTCGA C                                               743  
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792 (2) INFORMATION FOR SEQ ID NO: 10:  
793  
794       (i)       SEQUENCE CHARACTERISTICS:  
795               (A) LENGTH: 146 amino acids  
796               (B) TYPE: amino acid  
797               (D) TOPOLOGY: linear  
798       (ii)       MOLECULE TYPE: protein  
799  
800       (xi)       SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
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802 Val His Leu Thr Pro Glu Glu Lys Ser Ala Val Thr Ala Leu Trp Gly  
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806                               20                               25                               30  
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808 Val Val Tyr Pro Trp Thr Gln Arg Phe Phe Glu Ser Phe Gly Asp Leu  
809                               35                               40                               45  
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811 Ser Thr Pro Asp Ala Val Met Gly Asn Pro Lys Val Lys Ala His Gly  
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817 Leu Lys Gly Thr Phe Ala Thr Leu Ser Glu Leu His Cys Asp Lys Leu  
818                               85                               90                               95  
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820 His Val Asp Pro Glu Ser Phe Arg Leu Leu Gly Asn Val Leu Val Cys  
821                               100                               105                               110  
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823 Val Leu Ala His His Phe Gly Lys Glu Phe Thr Pro Pro Val Gln Ala  
824                               115                               120                               125  
825  
826 Ala Tyr Gln Lys Val Val Ala Gly Val Ala Asn Ala Leu Ala His Lys  
827       130                               135                               140  
828  
829 Tyr His  
830       145  
831  
832



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833 (2) INFORMATION FOR SEQ ID NO:11:

834

835 (i) SEQUENCE CHARACTERISTICS:

836 (A) LENGTH: 17 amino acids

837 (B) TYPE: amino acid

838 (D) TOPOLOGY: linear

839

840 (ii) MOLECULE TYPE: peptide

841

842 (v) FRAGMENT TYPE: N-terminal

843

844 (vi) ORIGINAL SOURCE:

845 (A) ORGANISM: alkalophilic Bacillus sp.

846 (B) STRAIN: 38-2

847

848 (vii) IMMEDIATE SOURCE:

849 (B) CLONE: beta-cyclodextrin

850

851 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

852

853 Ala Pro Asp Thr Ser Val Ser Asn Lys Gln Asn Phe Ser Thr Asp Val

854 1 5 10 15

855

856 Ile

PAGE: 1

SEQUENCE VERIFICATION REPORT  
PATENT APPLICATION US/07/923,692A

DATE: 05/20/93  
TIME: 11:43:21  
S4493

LINE ERROR

ORIGINAL TEXT

31 Wrong application Serial Number  
601 Entered and Calc. Seq. Length differ

(A) APPLICATION NUMBER: US 923,692  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO

PAGE: 1

SEQUENCE MISSING ITEM REPORT  
PATENT APPLICATION US/07/923,692A

DATE: 05/20/93  
TIME: 11:43:21  
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MANDATORY IDENTIFIER THAT WAS NOT FOUND

COUNTRY

PRIOR APPLICATION DATA

More Identifiers Found Than Max Allowed

PAGE: 1

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PATENT APPLICATION US/07/923,692A

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CORRECTED TEXT